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concluded

34. (Amended) The cut flower from a transgenic plant according to claim 33.

35. (Amended) The seed from a transgenic plant according to claim 33.

36. (Amended) The fruit from a transgenic plant according to claim 33.

37. (Amended) The leaf from a transgenic plant according to claim 33.

### REMARKS

In the Office Action dated November 3, 2000, claims 1-29 are pending.

In response to the Office Action, Applicants have amended the claims, which when considered in view of the following remarks, is deemed to place the application in condition for allowance. Favorable consideration of all pending claims is respectfully requested.

In the Office Action, the Examiner indicates that the present application fails to fully comply with the sequence rules under 37 C.F.R. §§1.821-1.825. Specifically, the Examiner points out that sequences disclosed at page 20, lines 11, 12 and 14 and in Table 7 are not identified with SEQ ID NOS.

It is respectfully submitted that a substitute Sequence Listing will be provided in due course which listing will include the sequences disclosed at page 20, lines 11, 12 and 14 and in Table 7, and that the SEQ ID NOS for these sequences will be inserted into the specification.

The Examiner has made the restriction requirement final. Consequently, claims 1-24 and 26-39 are under consideration. The non-elected claim 25 is withdrawn from consideration.

In this regard, Applicants have canceled claim 25 without prejudice by way of the foregoing amendment. Applicants reserve the right to file a divisional application to pursue the subject matter of claim 25.

Claims 38-39 are rejected under 35 U.S.C. §101 as allegedly directed to non-statutory matter. The Examiner contends that the claims, drawn to the "use" of an isolated nucleic acid molecule, is directed to non-statutory matter.

It is respectfully submitted that claims 38-39 have been canceled without prejudice. Applicants reserve the right to file a continuation application to pursue the subject matter of canceled claims 38-39.

Claims 1-24 and 26-39 are rejected under 35 U.S.C. § 112, first paragraph, as allegedly containing subject matter not described in the specification in such a way as to convey to one skilled in the art that the inventors had possession of the claimed invention at the time the application was filed.

The Examiner admits that the specification teaches nucleic acid molecules encoding enzymes with flavonoid hydroxylase activity from a variety of ornamental plants. However, the Examiner contends that the specification does not teach any nucleic acid molecule encoding a F3'H which modulates hydroxylation of flavonoid compounds more efficiently than the F3'H encoded by SEQ ID NO: 26.

In response, Applicants respectfully submit that the specification teaches a number of nucleic acid molecules encoding a F3'H which effects hydroxylation of flavonoid compounds more efficiently than the F3'H encoded by SEQ ID NO: 26.

In this regard, it is respectfully submitted that SEQ ID NO: 26 has been described by Holton et al. (WO 93/20206) as encoding a petunia F3'H of 496 amino acids. SEQ ID NO: 26, when introduced into SKr4xSW63 petunias (see the construct pCGP809 in Holton et al.) resulted in color changes to parts of the petal. The color changes are described as changing from 55D-56C/D to 54A-55A. See Holton et al. (WO 93/20206), particularly at pages 33, line 22 to page 34, line 5.

In contrast, the petunia F3'H sequence SEQ ID NO: 1 of the present invention (encoding a F3'H of 512 amino acids), when inserted in the construct pCGP1867 (mac:petunia OGR-38:mas) (which utilizes the same promoter and terminator combination as for pCGP809 of Holton et al. reference) and introduced into the SKr4xSW63 petunia, resulted in a more dramatic color change to the whole of the corolla. The color changes have been described as changing from a very pale lilac (69B/73D) to dark pink (67B, 68A). In addition, the anther and pollen of

the transgenic flowers also showed a dramatic change in color from white to pink (see pages 47-48 and Table 5 of the specification). TLC analysis of the anthocyanins in the transgenic petals revealed the production of the 3'-hydroxylated cyanidin and its derivative peonidin as well as the 3'-hydroxylated flavonol, quercetin (see page 50 and Table 6 of the specification). In addition, the rose, snapdragon and carnation F3'H clones (SEQ ID NO: 14, SEQ ID NO: 5 and SEQ ID NO: 3), when introduced into the SKr4xSW63 petunias, result in similar dramatic color changes to the whole of the corolla and to the anthers and pollen (see pages 55, 67 and 80 of the specification).

Thus, it is respectfully submitted that, contrary to the Examiner's allegation, the specification teaches a number of nucleic acid molecules encoding a F3'H wherein the F3'H effects hydroxylation of flavonoid compounds more efficiently than the F3'H encoded by SEQ ID NO: 26.

The Examiner further alleges that the specification does not teach nucleic acid molecules which are "derivatives" of specifically described nucleic acid molecules, or nucleic acid molecules which share sequence similarities or which hybridize to the specifically described nucleic acid molecules.

In this regard, Applicants respectfully submit that the specification adequately teaches "derivatives" of the specifically described nucleic acid molecules. See particularly pages 12-13 of the specification. However, in an effort to favorably advance the prosecution of the present application, Applicants have amended the claims to delete the term "derivative" and "functional derivative". Applicants reserve the right to file a continuation application to pursue subject matter relating to such "derivatives" and "functional derivatives" and the use thereof.

Furthermore, Applicants respectfully submit that the specification describes nucleic acid molecules encoding a F3'H from a large number of ornamental plant species. These nucleic acid molecules share significant sequence homologies with each other and were isolated based on hybridization methodologies.

In view of the foregoing, it is respectfully submitted that the nucleic acid molecules of claims 1-24 and 26-37 are adequately described in the specification in a manner which fully complies with the written description requirement of 35 U.S.C. §112, first paragraph. Accordingly, withdrawal of the rejection under 35 U.S.C. §112, first paragraph is respectfully requested.

Claims 1-24 and 26-39 are rejected under 35 U.S.C. §112, first paragraph as allegedly not enabled.

The Examiner contends that the specification is enabling only for an isolated nucleic acid molecule encoding a plant F3'H, a gene construct and transgenic plant comprising such nucleic acid molecule, a method for altering F3'H activity and flower color alteration in transgenic plants using such nucleic acid molecule. However, the Examiner contends that the specification is not enabling for the subject matter as claimed. In particular, the Examiner alleges that the specification does not teach any nucleic acid molecule encoding a F3'H which modulates hydroxylation of flavonoid compounds more efficiently than the F3'H encoded by SEQ ID NO: 26. In addition, the Examiner alleges that the specification does not teach nucleic acid molecules which are "derivatives" of specifically described nucleic acid molecules, or nucleic acid molecules which share sequence similarities or which hybridize to the specifically described nucleic acid molecules.

As submitted above, the specification teaches a number of nucleic acid molecules encoding a F3'H which effects hydroxylation of flavonoid compounds more efficiently than the F3'H encoded by SEQ ID NO: 26. The specification also teaches nucleic acid molecules that share sequence similarities and hybridize to the specifically described nucleic acid molecules. In addition, the claims have been amended to delete the term "derivative" or "functional derivative". Applicants respectfully submit that, in light of the present teaching, those skilled in the art can make and use the claimed invention without undue experimentation. As such, the rejection under the enablement requirement of 35 U.S.C. §112, first paragraph, is obviated. Withdrawal of the rejection is therefore respectfully requested.

Claims 1-24 and 26-39 are rejected under 35 U.S.C. §112, second paragraph as allegedly indefinite.

In particular, the Examiner contends that the terms “derivative” and “functional derivative” as recited in the claims are indefinite. Applicants respectfully submit that these terms are defined in the specification and the meaning of these terms is clear to those skilled in the art. See, e.g., pages 12-13 for “derivative”. However, in an effort to favorably advance the prosecution of the present application, Applicants have amended the claims to delete the term “derivative” and “functional derivative”. Applicants reserve the right to file a continuation application to pursue subject matter relating to such “derivatives” and “functional derivatives” as well as the use of such “derivatives” and “functional derivatives”.

Claims 1-24 and 26-37 have also been amended to address other indefiniteness alleged by the Examiner. It is respectfully submitted that claims 1-24 and 26-37 as presently recited are not indefinite. Such amendment to the claims is fully supported by the specification. No new matter is introduced.

In view of the amendment to claims 1-24 and 26-37 and the cancellation of claims 38-39, the rejection of claims 1-24 and 26-39 under 35 U.S.C. §112, second paragraph, is overcome. Withdrawal of the rejection is respectfully requested.

Claims 1-24 and 26-39 are rejected under 35 U.S.C. §102(b) as allegedly anticipated by Holton et al. (WO 93/20206).

Applicants respectfully submit that Holton et al. disclose a nucleic acid molecule which appears to be identical to SEQ ID NO: 26 discussed in the present application and which encodes a petunia F3'H. However, Holton et al. do not teach any nucleic acid molecule which encodes a F3'H which effects *more efficient* hydroxylation of flavonoid compounds than does the F3'H encoded by SEQ ID NO: 26. Accordingly, Holton et al. do not teach the present invention.

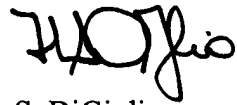
The rejection of claims 1-24 and 26-39 under 35 U.S.C. §102(b) as allegedly anticipated by Holton et al. is overcome. Withdrawal of the rejection is respectfully requested.

Claims 2-24, 29-30, 32 and 34-37 are also objected to for allegedly improper use of articles. It is respectfully submitted that these claims have been amended to use the proper articles.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment, which is captioned **"Version with markings to show changes made."**

In view of the foregoing amendments and remarks, it is firmly believed that the subject application is in condition for allowance, which action is earnestly solicited.

Respectfully submitted,



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Encl.: Version with Markings to Show Changes Made



Appln. No. 09/142,108

Date: May 3, 2001

**Version With Markings to Show Changes Made**

**IN THE CLAIMS:**

Claims 25 and 38-39 have been canceled without prejudice.

Claims 1-24 and 26-37 have been amended as follows:

1. (Amended) An isolated nucleic acid molecule comprising a sequence of nucleotides encoding a flavonoid 3'-hydroxylase [or a derivative thereof] wherein said flavonoid 3'-hydroxylase [or its derivative is capable of] effects more efficient [modulation of] hydroxylation of flavonoid compounds in plants than [is] a flavonoid 3'-hydroxylase encoded by the nucleotide sequence set forth in SEQ ID NO: 26.

2. (Amended) [An] The isolated nucleic acid molecule according to claim 1 comprising a nucleotide sequence which [corresponds] maps to the genetic locus designated *Ht1* or *Ht2* in petunia or to loci in other flowering plant species which contain sequences coding for proteins which control production of 3'-hydroxylated flavonoids.

3. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO:1, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 1, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO:1 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

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4. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 3, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 3, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO:3 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

5. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 5, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 5, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO: 5 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

6. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 7, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 7, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO: 7 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

7. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary

nucleotide sequence substantially] as set forth in SEQ ID NO: 9, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 9, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO: 9 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

8. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 14, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 14, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO: 14 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

9. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 16, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 16, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO: 16 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

10. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 18, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 18, or [capable of hybridizing to the sequence set forth

in] hybridizes to SEQ ID NO: 18 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

11. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 20, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 20, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO: 20 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

12. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 22, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 22, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO: 22 under low stringency conditions, wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

13. (Amended) [An] The isolated nucleic acid molecule according to claim 2, wherein said nucleic acid molecule comprises [comprising] a nucleotide sequence [or complementary nucleotide sequence substantially] as set forth in SEQ ID NO: 24, or [having] has at least about 60% similarity [thereto] to SEQ ID NO: 24, or [capable of hybridizing to the sequence set forth in] hybridizes to SEQ ID NO: 24 under low stringency conditions, wherein said conditions

comprise hybridization at 42 °C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

14. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 2 or an amino acid sequence having at least about 50% similarity thereto.

15. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 4 or an amino acid sequence having at least about 50% similarity thereto.

16. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 6 or an amino acid sequence having at least about 50% similarity thereto.

17. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 8 or an amino acid sequence having at least about 50% similarity thereto.

18. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 10 or SEQ ID NO:11 or SEQ ID NO:12 or SEQ ID NO:13 or an amino acid sequence having at least about 50% similarity thereto.

19. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 15 or an amino acid sequence having at least about 50% similarity thereto.

20. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 17 or an amino acid sequence having at least about 50% similarity thereto.

21. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 19 or an amino acid sequence having at least about 50% similarity thereto.

22. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 21 or an amino acid sequence having at least about 50% similarity thereto.

23. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid sequence [substantially] as set forth in SEQ ID NO: 23 or an amino acid sequence having at least about 50% similarity thereto.

24. (Amended) [An] The isolated nucleic acid molecule according to claim 2 comprising  
----- a sequence of nucleotides encoding or complementary to a sequence encoding an amino acid -----

sequence [substantially] as set forth in SEQ ID NO: 25 or an amino acid sequence having at least about 50% similarity thereto.

26. (Amended) A genetic construct capable of reducing expression of an endogenous gene encoding a flavonoid 3'-hydroxylase in a plant, said genetic construct comprising a nucleotide sequence selected from the group consisting of:

- (iii) a nucleotide sequence encoding [an] the amino acid sequence set forth in one of SEQ ID NO:2, [4, 6, 8, 10, 11, 12, 13, 15, 17, 19, 21, 23 or 25 or a complementary form thereof] SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, or SEQ ID NO: 25;
- (iv) [a] the nucleotide sequence set forth in one of SEQ ID NO: 1, [3, 5, 7, 14, 16, 18, 20, 22 or 24], SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22 or SEQ ID NO: 24, or the coding region in SEQ ID NO: 9 [or a complementary form thereof];
- (iii) a nucleotide sequence having at least about 60 % similarity to (i) or (ii); and
- (iv) a nucleotide sequence [capable of hybridizing] which hybridizes under low stringency conditions to (i), (ii) [and/or] or (iii) wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

27. (Amended) A method for producing a transgenic plant [capable of synthesizing] which synthesizes a flavonoid 3'-hydroxylase [or a functional derivative thereof], said method comprising stably transforming a cell of a [suitable] plant with a nucleic acid molecule which comprises a sequence of nucleotides encoding said flavonoid 3'-hydroxylase [or a derivative thereof] under conditions [permitting the eventual expression of] wherein said nucleic acid molecule is expressed, regenerating a transgenic plant from the cell, and growing said transgenic plant for a time and under conditions [sufficient to permit the expression of] wherein the nucleic acid molecule is expressed.

28. (Amended) A method for producing a transgenic plant with reduced endogenous [or existing] flavonoid 3'-hydroxylase activity, said method comprising stably transforming a cell of a [suitable] plant with a nucleic acid molecule which comprises a sequence of nucleotides encoding or complementary to a sequence encoding flavonoid 3'-hydroxylase [or a derivative thereof], regenerating a transgenic plant from the cell, and [where necessary] growing said transgenic plant under conditions [sufficient to permit the expression of] wherein the nucleic acid molecule is expressed.

29. (Amended) [A] The method according to claim 27 or 28 wherein [the introduced] said nucleic acid molecule comprises a nucleotide sequence or complementary nucleotide sequence selected from:

- (i) a nucleotide sequence encoding [an] the amino acid sequence set forth in one of SEQ ID NO:2, [4, 6, 8, 10, 11, 12, 13, 15, 17, 19, 21, 23 or 25 or a complementary form thereof] SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO:

15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, or SEQ ID NO: 25;

- (ii) [a] the nucleotide sequence set forth in one of SEQ ID NO: 1, [3, 5, 7, 14, 16, 18, 20, 22 or 24], SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22 or SEQ ID NO: 24, or the coding region in SEQ ID NO: 9 [or a complementary form thereof];
- (iii) a nucleotide sequence having at least about 60 % similarity to (i) or (ii); and
- (iv) a nucleotide sequence [capable of hybridizing] which hybridizes under low stringency conditions to (i), (ii) [and/or] or (iii) wherein said conditions comprise hybridization at 42 °C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

30. (Amended) [A] The method according to claim 27 or 28 wherein [the recipient] said plant is selected from the group consisting of petunia, carnation, chrysanthemum, rose, snapdragon, tobacco, cornflower, pelargonium, lisianthus, gerbera, apple, iris, lily, African violet and morning glory.

31. (Amended) A method for producing a transgenic plant capable of modulating hydroxylation of flavonoid compounds, said method comprising stably transforming a cell or group of cells of a [suitable] plant with a nucleic acid molecule comprising a sequence of nucleotides encoding, or complementary to a sequence encoding, flavonoid 3'-hydroxylase [or a derivative thereof], and regenerating a transgenic plant from said cell or group of cells.

32. (Amended) [A] The method according to claim 31 where the transformed nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of:

- (i) a nucleotide sequence encoding [an] the amino acid sequence set forth in one of SEQ ID NO:2, [4, 6, 8, 10, 11, 12, 13, 15, 17, 19, 21, 23 or 25 or a complementary form thereof] SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, or SEQ ID NO: 25;
- (ii) [a] the nucleotide sequence set forth in one of SEQ ID NO: 1, [3, 5, 7, 14, 16, 18, 20, 22 or 24], SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22 or SEQ ID NO: 24, or the coding region in SEQ ID NO: 9 [or a complementary form thereof];
- (iii) a nucleotide sequence having at least about 60 % similarity to (i) or (ii); and
- (iv) a nucleotide sequence [capable of hybridizing] which hybridizes under low stringency conditions to (i), (ii) [and/or] or (iii) wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

33. (Amended) A transgenic plant having tissue exhibiting altered colour, said transgenic plant comprising a nucleic acid molecule comprising a sequence of nucleotides selected from the group consisting of:

- (i) a nucleotide sequence encoding [an] the amino acid sequence set forth in one of -----  
SEQ ID NO:2, [4, 6, 8, 10, 11, 12, 13, 15, 17, 19, 21, 23 or 25 or a

complementary form thereof] SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, or SEQ ID NO: 25;

- (ii) [a] the nucleotide sequence set forth in one of SEQ ID NO: 1, [3, 5, 7, 14, 16, 18, 20, 22 or 24], SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22 or SEQ ID NO: 24, or the coding region in SEQ ID NO: 9 [or a complementary form thereof];
- (iii) a nucleotide sequence having at least about 60 % similarity to (i) or (ii); and
- (iv) a nucleotide sequence [capable of hybridizing] which hybridizes under low stringency conditions to (i), (ii) [and/or] or (iii) wherein said conditions comprise hybridization at 42°C in about 1% to about 15% formamide and about 1M to about 2M salt, and washing with about 1M to about 2M salt.

34. (Amended) [A] The cut flower from a transgenic plant according to claim 33.

35. (Amended) [A] The seed from a transgenic plant according to claim 33.

36. (Amended) [A] The fruit from a transgenic plant according to claim 33.

37. (Amended) [A] The leaf from a transgenic plant according to claim 33.